

[illegible]

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Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
50 55 60

ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag	ccc	atc	atc	ttc	aca	ggg	241
Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	Pro	Ile	Ile	Phe	Thr	Gly	
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gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag	gag	gcc	atg	gga	gtc	ttt	289
Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	Glu	Ala	Met	Gly	Val	Phe	
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Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	Ser	Phe	Asp	Val	Glu	Leu	
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His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	Arg	Lys	Gln	Ile	Leu	Ala	
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Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	Ile	Gln	Glu	Val	Thr	Trp	
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Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser	
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Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	Lys	Lys	Lys	Asn	Pro	Phe	
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tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	att	tgc	ata	tgt	aat	gag	577
Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	Ile	Cys	Ile	Cys	Asn	Glu	
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Glu	Leu	Asn	Val	Asn	Pro	Gln	Asp	Asn	Gly	Glu	Asn	Ile	Ser	Trp	Thr	
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Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	Ser	Leu	Ala	Trp	Arg	Pro	
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Arg 225	Arg	Lys	Trp	Phe	Cys 230	Gly	Thr	Gly	Pro	Gly 235	Ser	Leu	Cys	Cys	Val 240	
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cca Pro	tct Ser	agt Ser	aga Arg	gct Ala	gtg Val	aga Arg	aga Arg	agt Ser	cca Pro	cca Pro	tcc Ser	tcc Ser	aga Arg	ctc Leu	cag Gln	1057
			340					345					350			
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tac Tyr	aaa Lys	acc Thr	gta Val	gtg Val	gca Ala	gag Glu	ctg Leu	acc Thr	aag Lys	acc Thr	gtg Val	gga Gly	atc Ile	tac Tyr	ctc Leu	1201
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ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat 1249
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 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
 420 425 430

ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc 1345
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
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<210> 2

<211> 459

<212> PRT

<213> Homo sapiens

<400> 2

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Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	Gly	Glu	Ile	Ser	Glu	Met
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Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg	Ser	Ala	Phe	Thr	Val	Lys
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Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	Pro	Ile	Ile	Phe	Thr	Gly
65				70					75					80	
Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	Glu	Ala	Met	Gly	Val	Phe
			85					90					95		
Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	Ser	Phe	Asp	Val	Glu	Leu
			100					105					110		
His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	Arg	Lys	Gln	Ile	Leu	Ala
		115				120						125			
Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	Ile	Gln	Glu	Val	Thr	Trp
	130					135					140				
Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser
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00940-092660

Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe
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 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu
 180 185 190
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr
 195 200 205
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro
 210 215 220
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val
 225 230 235 240
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala
 245 250 255
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu
 260 265 270
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile
 275 280 285
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe
 290 295 300
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln
 305 310 315 320
 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
 325 330 335
 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
 340 345 350
 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
 355 360 365
 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
 370 375 380
 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
 385 390 395 400
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
 405 410 415
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
 420 425 430
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<211> 1377

<212> DNA

<213> Artificial Sequence

<223> Degenerate polynucleotide encoding a polypeptide
of SEQ ID NO:2

<222> (1)...(1377)

<223> Each n is independently A, T, G, or C.

 $\langle 222 \rangle$ (1) ... (1377)

$\langle 223 \rangle$ n = A, T, C or G

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ccngcncayc	cnmgncnc	ngargargtn	ggncncncg	gngcncncg	nytnccncar	120		
tayacngng	arathwsnga	ratgacnaar	tgyccntgyc	cngayathga	rmgnwsngcn	180		
ttyacngtna	arytnwsngg	naarytnccn	ytnccnttya	arccnathat	httyacnggn	240		
gtnytnaya	aygcncarmg	ngayytnaar	gargcnatgg	gngtnttygc	ntgymngtn	300		
ccnggnaayt	aytaywsnws	nttygaygt	garytncayc	aytgyaargt	naayathtg	360		
ytnatgmna	arcarathyt	ngcnaayaar	gargarathw	snaarcarca	rwnathcar	420		
gargtnacnt	gggtnytnyt	naargcntty	wsnttyathm	gngargcnga	rcayaarwsn	480		
wsngaraayy	tncayccnga	yaaygt	nath	aaraaraara	ayccnttyws	540		
ttyaarytng	cngcngarat	htgyathtg	y	aaygargary	tnaaygt	naa	yccncargay	600
aayggngara	ayathwsntg	gacntgycar	mgnwsnwsnc	arcarwsnat	haarwsnytn	660		
gcntggmgnc	cnmgnmgnaa	rtggtytgy	ggnacnggnc	cnggnwsnyt	ntgytgygt	720		
carccnmng	ayytngtncc	ntgygtncn	gt	naaywsng	cngtngcnws	ngarggngcn	780	
wsnccnaarc	cntggcaryt	nccnwsnggn	gtngarccng	tnggngcn	naa	raarwsnmgn	840	
athgargtnt	gggarccnc	nathmgntty	caraaratht	ayggnaaycc	ntggatgccn	900		
mgncaraart	tygcngtngg	ngtnggnwsn	wsntggmgna	cnwsngcnmg	ngtngtn	car	960	
aarggnaayg	tnggntggga	rcncncncay	mgngtnccnw	snggngcnc	nwsnwsnmgn	1020		
gcngtnmgnm	gnwsnccnc	nwsnwsnmgn	ytn	caraarg	gnmg	nwsnac	ngaywsnytn	1080
carcaygtnc	cngaraarws	nacngayacn	cartgycarc	cngt	naargc	ngcnggnatg	1140	
garwsngtnc	cntayaarac	ngtngtngcn	garytnacna	aracngtngg	nath	tayyt	1200	
ytncaytgyc	aygayytnga	ygtnmgncay	ggngt	naarm	gngaycaytt	yggngcnytn	1260	
mgnttygayt	gyccnacngg	nttymg	nacn	tayatgggnc	cngtnccnyt	ntgyttygg	1320	
carttyttyc	cnttygg	nac	ngcngtntty	acncartgyy	tntayyt	nca	ytgyatg	1377

<211> 31

<213> Artificial Sequence

<220>

<223> Aromatic motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan, or
leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(31)

<223> Each Xaa is independently any amino acid residue

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Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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<222> (1)...(1731)
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aaa tgc tgc att gga gag atg ggg tac atg cga gtg aca atg gga aga 96
Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg
20 25 30

gtt ggt agc tgg aga gaa ctg gga aag cct tca ggc atc tgg gaa atg 144
Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met
35 40 45

gct ggg gat aca gag gtg aag aag aca ggg ttt ctt cag gaa ctc act 192
Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr
50 55 60

ttc cag cag gag cct ggc atc tcc tcc tct cct tct tgc tcc cgc tct 240
Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser
65 70 75 80

tgc cat gtg aca cca cct gct cca cct gca tct tct gcc ata att gta 288
Cys His Val Thr Pro Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val
85 90 95

aga ttc ctg agg ccc tca cca gaa gca gat gcc agc agc atg ctt att 336
Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile
100 105 110

gca cag tct gta gaa ccg ata gtg gtc ata cct gtc tta ata acg gca 384
Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala
115 120 125

gtc att gag cat gta gaa gtt gct gga cct cca gca cac ccc aqg ccc 432

Val	Ile	Glu	His	Val	Glu	Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro	
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Pro	Glu	Glu	Val	Gly	Pro	Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	
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gga	gaa	ata	agt	gaa	atg	aca	aaa	tgc	ccc	tgt	cct	gat	ata	gaa	agg	528
Gly	Glu	Ile	Ser	Glu	Met	Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg	
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Ser	Ala	Phe	Thr	Val	Lys	Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	
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Pro	Ile	Ile	Phe	Thr	Gly	Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	
		195				200						205				
gag	gcc	atg	gga	gtc	ttt	gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc	672
Glu	Ala	Met	Gly	Val	Phe	Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	
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agc	ttt	gat	gtt	gag	ctg	cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg	720
Ser	Phe	Asp	Val	Glu	Leu	His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	
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Arg	Lys	Gln	Ile	Leu	Ala	Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	
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Ile	Gln	Glu	Val	Thr	Trp	Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	
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gag	gca	gag	cat	aag	agt	tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	864
Glu	Ala	Glu	His	Lys	Ser	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	
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Lys	Lys	Lys	Asn	Pro	Phe	Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	
	290					295					300					

att	tgc	ata	tgt	aat	gag	gag	ctg	aat	gtt	aat	cct	caa	gac	aat	ggg	960
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Glu	Asn	Ile	Ser	Trp	Thr	Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	
				325					330					335		
tca	ctg	gcc	tgg	agg	cct	agg	aga	aaa	tgg	ttt	tgt	ggg	aca	ggc	cca	1056
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Val	Asn	Ser	Ala	Val	Ala	Ser	Glu	Gly	Ala	Ser	Pro	Lys	Pro	Trp	Gln	
	370					375					380					
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Val	Trp	Glu	Pro	Pro	Ile	Arg	Phe	Gln	Lys	Ile	Tyr	Gly	Asn	Pro	Trp	
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Met	Pro	Arg	Gln	Lys	Phe	Ala	Val	Gly	Val	Gly	Ser	Ser	Trp	Arg	Thr	
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Ser	Ala	Arg	Val	Val	Gln	Lys	Gly	Asn	Val	Gly	Trp	Glu	Pro	Pro	His	
		435					440					445				
aga	gtc	ccc	agt	ggg	gct	cca	tct	agt	aga	gct	gtg	aga	aga	agt	cca	1392
Arg	Val	Pro	Ser	Gly	Ala	Pro	Ser	Ser	Arg	Ala	Val	Arg	Arg	Ser	Pro	
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<211> 577
<212> PRT
<213> Homo sapiens
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 35 40 45
 Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr
 50 55 60
 Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser
 65 70 75 80
 Cys His Val Thr Pro Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val
 85 90 95
 Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile
 100 105 110
 Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala
 115 120 125
 Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro
 130 135 140
 Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr
 145 150 155 160
 Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg
 165 170 175
 Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys
 180 185 190
 Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys
 195 200 205
 Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser
 210 215 220
 Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met
 225 230 235 240
 Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser
 245 250 255
 Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg
 260 265 270
 Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile
 275 280 285
 Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu
 290 295 300
 Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly
 305 310 315 320
 Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys
 325 330 335
 Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro
 340 345 350
 Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro
 355 360 365

09092610 11254
 11254

